

265TT-98TH468D

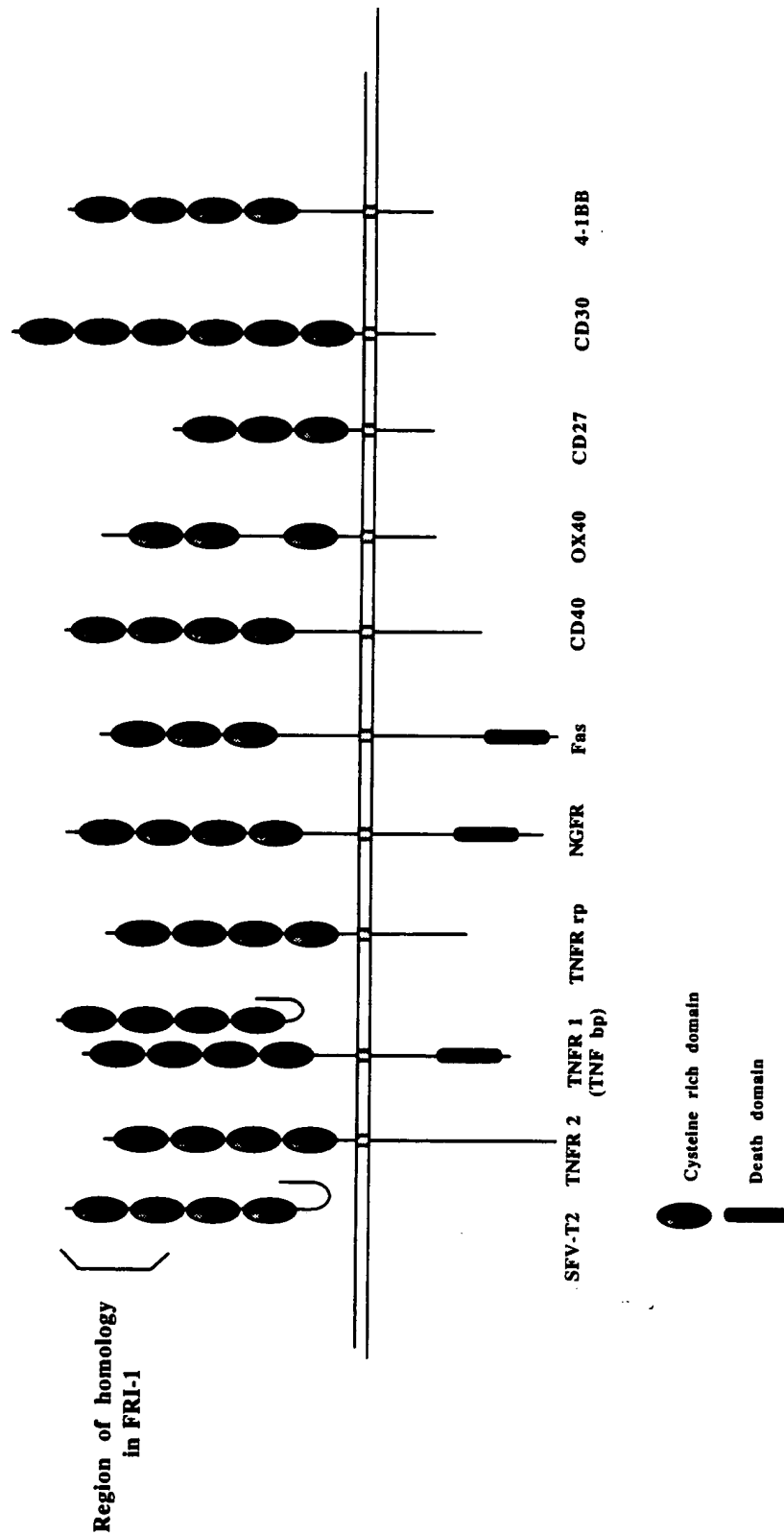
Figure 1A

```
148      178      208      238      268      298
FRI-1  , ALLVFLDIIEWTTQETFPKYLHYDPETGRQLLCDKCAPGTYLKQHC.TVRRKTLCV.PCPDY.SYTD
SW: TNR2_HUMAN  HALPAQVAFTPYAPEPGSTCRLREYVDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCED
              30      40      50      60      70      80
              YSYTDSWHTS
FRI-1  :||:|:
SW: TNR2_HUMAN  STYTQLWNWVPECLSCGSRCSDDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPL
              90      100     110     120     130     140
```

1B

```
FRI-1  69 YLHYDPETGRQLLCDKCAPGTYLKQHC.TVRRKTLCV.PCPDY.SYTD
TNFR profile  | | . . . | . | | | : | . | : | | : | . | .
              6 YHYDQNGRMCEECHMCQPGHFLVKHCKQPKRDTVCHKPCPEPGVTYTDW
FRI-1  116 H
TNFR profile  |
              56 H
              Z Score = 8.29
```

Figure 1C



AUG

2B

10 30 50
ATCAAAAGCGAGGCATACCTTCCTGTTCGCCAGACCTTATATAAAACGTCAATGTCGCCCTG
70 90 110
GGCAGCAGAGAAAGCACCTAGCACTGGCCACAGCGGTGCGCCCTGAGGTTCACAGAGGACC
130 150 170
ACAATGAACAAGTGGCTGTGCTGTGCACTCCTGGTGTCTTGGACATCATGTAATGGACA
M N K W L C C A C L L V F L D I I E W T
190 210 230
ACCCAGGAACCTTTCTCCAAAATACTTGCATTATGACCCAGAAACCGAGCTCAGCTC
T O E T F P P K Y L H Y D P E T G R Q C L
250 270 290
TTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAACAGCACTGCACAGTCAGGAGGAAG
L C D K C A P G T Y L K Q H C T V R R K
310 330 350
ACACTGTGTGTCCTTGCCTTCACTACTCTTATACAGACAGCTGGCACAGGAGTGTAAT
T L C V P C P D Y S Y T D S W H T S D E
370 390 410
TGC GTGTACTGCAGCCCGTGTGCAAGAACTGCAGACCGTGAACACAGGAGTGAACCCG
C V Y C S P V C K E L Q T V K Q E C M R
430 450 470
ACCCACAACCGAGTGTGCGAATGTGAGGAAGGGCGCTACCTGGAGCTCGAATTCGTCTG
T H N R V C E C E E G R Y L E L E F C L
490 510 530
AAGCACCGGAGCTGTCCCGGAGCTTGGGTGTGCTGCAAGCTGGGACCCCGAGCGAAAC
K H R S C P P G L G V L Q A G T P E R N
550 570 590
ACGGTTGTCAAAGATGTCCGGATGGGTCTTCTCTCAGGTGAGACGTCTGAAAGCACCC
T V C K R C P D G F F S G E T S S K A P
610 630 650
TG TAGGAACACACCAACTGCAGCTCACTTGGCCCTCTGCTAATTCAGAAAGGAATGCA
C R K H T M C S S L G L L L I Q K G M A
670 690 710
ACACATGACAAATGTGTCGGAAGAACAGAACTCAAATTCGTGGAATAGATGTCT
T H D N V T C S G N R E A T Q N C G I D V
730 750 770
ACCCGTGCGGAAGGCATTCTTCAGGTTTGTGTGCTACCAAGATTATACCGAATTGG
T L C E E A F F R F A V P T K I I P N W
790 810 830
CTGAGTGTCTTGGTGGACAGTTTGCCTGGGACCAAGTGAATGCAGAGAGTGTAGAGAGG
L S V L V D S L P G T K V N A E S V E R
850 870 890
ATAAACCGGAGACAGCTCGCAAGAGCAAACTTTCCAGCTACTTAAGCTGTGGAAGCAT
I K R R H S S Y T Q T F Q L L K L W K H
910 930 950
CAAAACAGAGACAGCAAGAAATGGTGAAGAAGATCATCCAAGACATTGACCTCTGTGAAAGC
Q N R D Q E M V K K I I Q D I D L C E S
970 990 1010
AGTGTGCAACGGCATATCGGCCACGGGAACCTACCACAGAGCAGCTCCGCATCTTGATG
S V Q R H I G H A M L T T E Q L R I L M
1030 1050 1070
GAGAGCTTGGCTGGGAAGAAGATCAGCCCGACAGAGATTGAGAGAACGAGAAGACCTGC
E S L P G K K I S P D E I E R T R K T C
1090 1110 1130
AAACCCAGCGAGCAGCTCTCTGAAGCTACTGAGCTTGTGGAGGTCAAAAATGGAGACCAA
K P S E Q L L K L L S L W R I K N G D Q
1150 1170 1190
GACACCTTGAAGGGCTGTATGTACGCACCTCAAGCACTTGAAGCATACCACCTTTCCCAA
D T L K G L M Y A L K H L K A Y H F P K
1210 1230 1250
ACCGCTACCCACAGCTGTAGGAAGACCATCAGGTTCTTGCACAGCTTACCATGTACCGA
T V T H S L R K K T I R F L H S F T M Y R
1270 1290 1310
TTGTATCAAGAACTCTTTCTAGAAATGATAGGGAATCAGGTTCAACTGAGTGAAGATAAGC
L Y Q K L F L E M I G N Q V Q S V K I S
1330 1350 1370
TGCTTATAGTTAGGAATGGTCACTGGGCTGTTTCTTCAGGATGGGCAACACTGATGGAG
C L
1390 1410 1430
CAGATGGCTGCTTCTCCGGCTCTTGAATGGCAGTTGATTCTTCTCATCAGTTGGTGG
1450 1470 1490
GAATGAAGATCTCTCAGCCCAACACACACACTGGGGAGTCTGAGTCAGGAGAGTGAAGCA
1510 1530 1550
GGCTATTGTGTAATTTGTGCAAGCTGCGCAGGTGTACACCTAGAAAGCTCAAGCACCCCTGAG
1570 1590 1610
AAAGAGGATATTTTATAACCTCAAACTATAGGCCCTTCTCTCTCTTATGGATGAG
1630 1650 1670
TACTCAGAAGGCTTCTACTATCTTCTGTGTCACTCCCTAGATGAAGGCTCTTTTATTTAT
1690 1710 1730
TTTTTTATTCTTTTTTCGGAGCTGGGGACCGAACCAGGGCCTTGCAGCTTGCAGGGCAA
1750 1770 1790
GTGCTCTACCACTGAGCTAAATCTCCAACCCCTGAAGGCCCTTCTTCTTCTGCTCTGAT
1810 1830 1850
AGTCTATGACATTCTTTTTTCTACAATTCGTATCAGGTGCACGAGCTTATCCCATTTGT
1870 1890 1910
AGGTTTCTAGGCAAGTTGACCGTTAGCTATTTTTCCCTCTGAAGATTGAGATTCGAGTTGC
1930 1950 1970
AGACTTGGCTAGACAAGCAGGGGTAGGTTATGGTAGTTTATTTAACAAGACTGCCACCAGG
1990 2010 2030
AGTCCAGGTCTTCTTGTCTCTCTGTAGTTGTACCTAAGCTGACTCCAAGTACATTTAGTA
2050 2070 2090
TGAAAAATTAATCAACAAATTTTATTCTTCTATCAACATTGGCTAGCTTTGTTTCAGGGC
2110 2130 2150
ACTAAAAAGAACTACTATATGGAGAAGAAATGTATATGCCCCAACGTTTCAACAACCCA
2170 2190 2210
ATAGTTTATCCAGCTGTATGCTGGTTCAGTGTCTACTGACTATGGCCCTCTTATTAC
2230 2250 2270
TGCATGCAGTAATCAACTGGAAATAGTAATAATAATAAGAAATAAACTAGACTCC
2290 2310 2330
ATTGGATCTCTCTGAATATGGGAATATCTCAACTTAAGAAGCTTTGAGATTTCAGTTGT
2350 2370 2390
TAAAGGCTTTTATTAAGAAAGCTGATGCTCTTCTGTAAAGTTACTAATATATCTGTAAGA
2410 2430
CTATTACAGTATTGCTATTATATCATCCAG



fas.frg	M	L	G	I	W	T	-	-	-	L	L	P	L	V	L	T	S	-	V	A	R	L	S	S	K	S	V	N	A	Q	V	T	D	I	N	S	K	G	L	E	L	R	K	T	V	T	V	E	45			
tnfr1.frg	-	M	G	L	S	T	V	P	D	L	L	P	L	V	L	L	E	L	L	V	G	I	Y	P	S	G	V	I	G	L	V	P	H	-	-	-	-	L	G	D	R	E	K	R	D	S	V	N	C	44		
sfv-t2.frg	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	L	R	L	I	A	L	L	V	C	V	V	Y	-	V	Y	L	G	D	D	V	P	Y	S	N	Q	25	
tnfr2.frg	-	-	-	-	-	-	-	-	-	-	M	A	P	V	A	V	W	A	A	L	A	V	G	L	E	L	W	A	A	A	H	A	L	P	A	Q	V	A	F	T	P	Y	A	P	E	P	G	S	T	39		
cd40.frg	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	V	S	L	P	R	L	C	A	L	W	G	C	L	L	T	A	V	H	L	G	Q	C	V	T	C	S	D	28			
osteo.frg	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	N	K	W	L	C	C	A	L	L	V	F	L	D	I	I	E	W	T	T	Q	E	T	F	P	P	26		
ngfr.frg	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	G	A	G	A	T	G	R	A	M	D	G	P	R	L	L	L	L	L	L	G	V	S	L	G	-	G	A	K	E	A	C	P	T	34		
ox40.frg	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	Y	V	W	V	Q	Q	P	T	A	F	L	L	L	L	G	L	S	L	G	V	T	V	K	L	N	C	V	K	28
41bb.frg	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	G	N	N	C	Y	N	V	V	V	I	V	L	L	L	V	G	C	E	K	V	N	G	A	V	O	25	

[illegible]

Gene	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523
------	---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

fas.frg	-	C	R	L	C	D	E	G	H	G	L	E	V	E	I	N	C	T	R	T	Q	N	T	V	C	R	C	K	P	N	F	F	C	N	S	T	V	C	E	H	C	D	N	P	C	T	K	S	E	H	G	152
tnfr1.frg	N	C	S	L	C	L	N	G	-	-	-	T	V	H	L	S	C	Q	E	K	Q	N	T	V	C	R	C	H	A	G	G	F	F	L	R	E	N	E	C	V	S	C	D	N	C	K	P	S	E	H	G	191
sfv-t2.frg	-	-	-	-	-	P	C	T	G	H	L	S	E	S	Q	P	C	D	R	T	H	D	R	V	C	N	C	S	T	G	N	Y	C	L	L	K	G	Q	N	G	C	R	I	C	A	P	Q	T	K	E	C	129
tnfr2.frg	-	-	-	-	-	R	C	S	S	D	O	V	E	T	Q	A	C	T	R	E	Q	N	R	I	C	T	C	R	P	G	W	Y	C	A	L	S	K	Q	E	G	C	R	L	C	A	P	L	R	K	E	C	143
cd40.frg	-	-	-	-	-	-	N	Q	G	L	O	T	V	K	E	G	C	N	R	T	H	N	D	R	V	C	E	C	E	E	G	R	Y	-	-	-	L	E	L	E	-	-	A	C	A	Q	H	T	P	S	C	125
osteo.frg	-	-	-	-	-	V	C	K	L	O	T	V	K	E	G	C	N	R	T	H	N	D	R	V	C	E	C	E	E	G	R	Y	-	-	-	L	E	L	E	-	-	F	R	C	E	A	C	H	R	S	C	124
ngfr.frg	-	-	-	-	-	V	G	L	Q	S	M	-	-	S	A	P	C	C	V	E	A	D	D	A	V	C	R	C	A	Y	-	-	-	-	-	Q	D	E	-	T	T	G	R	C	E	A	C	H	R	S	C	128
ox40.frg	-	-	-	-	-	R	S	G	S	E	L	-	-	K	Q	N	C	T	P	T	E	D	T	V	C	Q	C	-	-	-	-	-	-	-	-	R	P	G	T	Q	P	R	Q	D	S	S	H	-	-	116		
41bb.frg	-	-	-	-	-	V	C	A	G	Y	F	R	F	K	K	F	C	S	S	T	H	N	A	E	C	E	C	I	E	G	F	H	C	L	G	P	Q	C	T	R	C	-	-	-	-	E	K	D	C	105		

fas.frg	-	-	-	-	I	K	E	C	T	L	T	S	N	T	K	C	K	E	-	-	-	-	-	E	G	S	R	S	N	L	-	-	-	G	W	L	C	L	L	L	L	P	I	P	L	I	187					
tnfr1.frg	-	-	-	-	T	K	L	C	L	P	Q	I	E	N	V	K	G	T	E	-	-	-	-	-	-	D	S	G	T	T	V	L	L	P	L	V	I	F	G	L	L	L	L	S	L	L	F	I	230			
sfv-t2.frg	P	A	G	Y	G	V	S	-	G	H	T	R	A	G	D	T	L	C	E	K	C	P	H	T	Y	S	D	S	L	S	P	T	E	R	C	G	T	S	F	N	Y	I	S	V	G	F	N	L	Y	178		
tnfr2.frg	R	P	G	F	G	V	A	R	P	G	T	E	T	D	V	V	C	K	P	C	A	P	G	T	T	F	S	N	T	S	S	L	T	D	I	C	R	P	H	Q	I	C	N	V	V	A	I	P	G	N	193	
cd40.frg	I	P	G	F	G	V	E	M	A	T	T	D	T	V	V	C	H	P	C	P	V	G	F	F	S	N	Q	S	S	L	F	E	K	C	Y	P	W	T	S	C	E	D	K	N	L	E	V	L	175			
osteo.frg	P	P	G	L	G	V	L	Q	A	G	T	P	E	R	N	T	V	C	E	K	C	P	D	G	G	T	F	S	G	E	T	S	S	H	V	A	P	C	R	K	H	T	N	C	E	S	D	L	E	R	L	174
ngfr.frg	E	A	G	S	G	L	V	F	S	C	Q	D	K	Q	N	T	V	C	E	E	C	P	D	G	T	F	S	P	G	E	A	N	S	K	V	A	P	C	L	P	C	T	V	C	E	S	D	T	G	Q	L	178
ox40.frg	-	-	-	-	-	-	-	-	-	-	-	K	L	G	V	D	C	V	P	C	P	P	G	H	F	S	P	G	S	N	-	Q	A	C	K	P	P	W	T	N	C	S	L	D	G	R	S	V	L	152		
41bb.frg	R	P	G	Q	E	L	T	K	Q	G	-	-	-	-	-	-	C	K	T	C	S	L	G	T	E	N	D	Q	-	N	G	T	G	V	C	R	P	P	W	T	N	C	S	L	D	G	R	S	V	L	147	

[illegible]

FIGURE 3

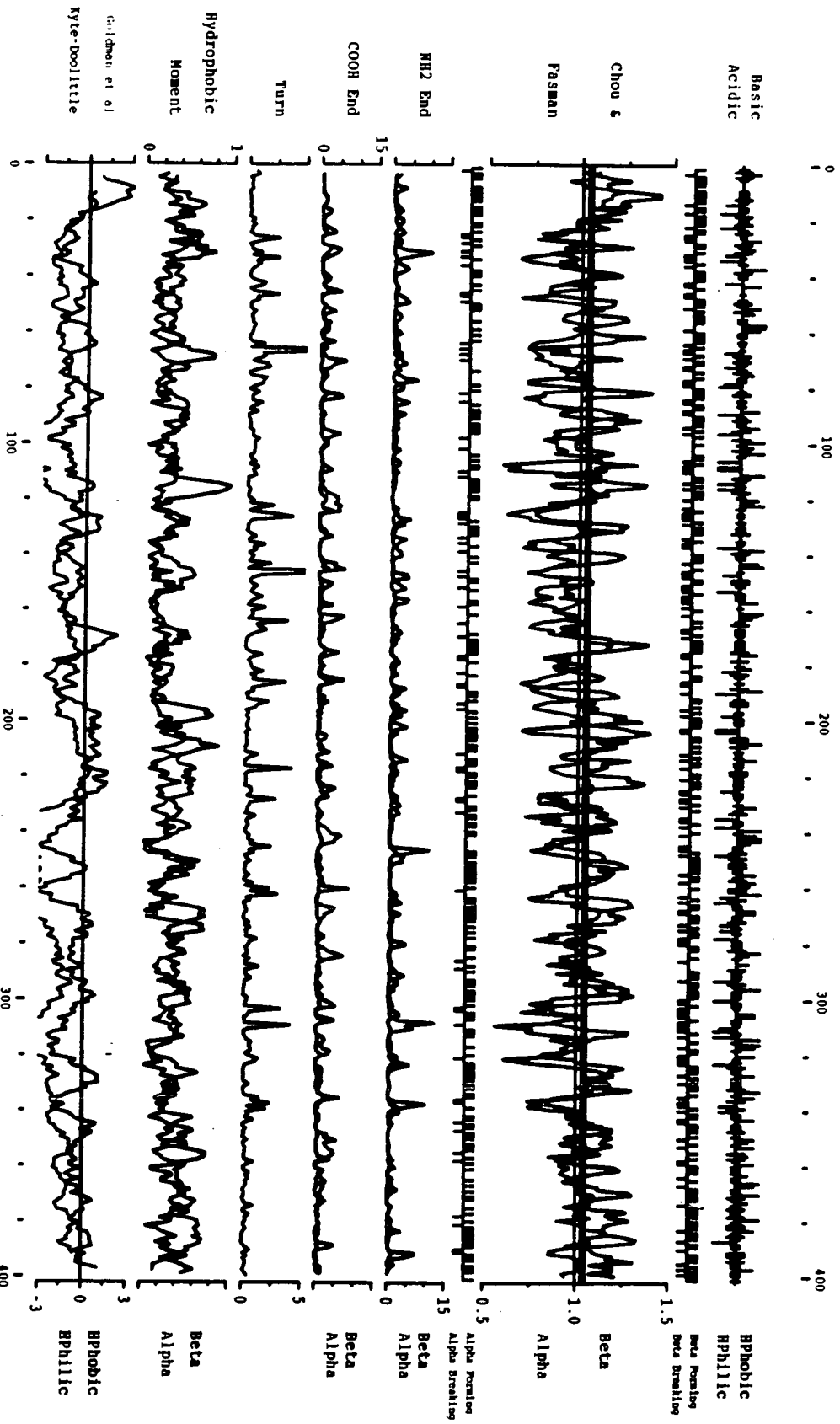


FIGURE 4

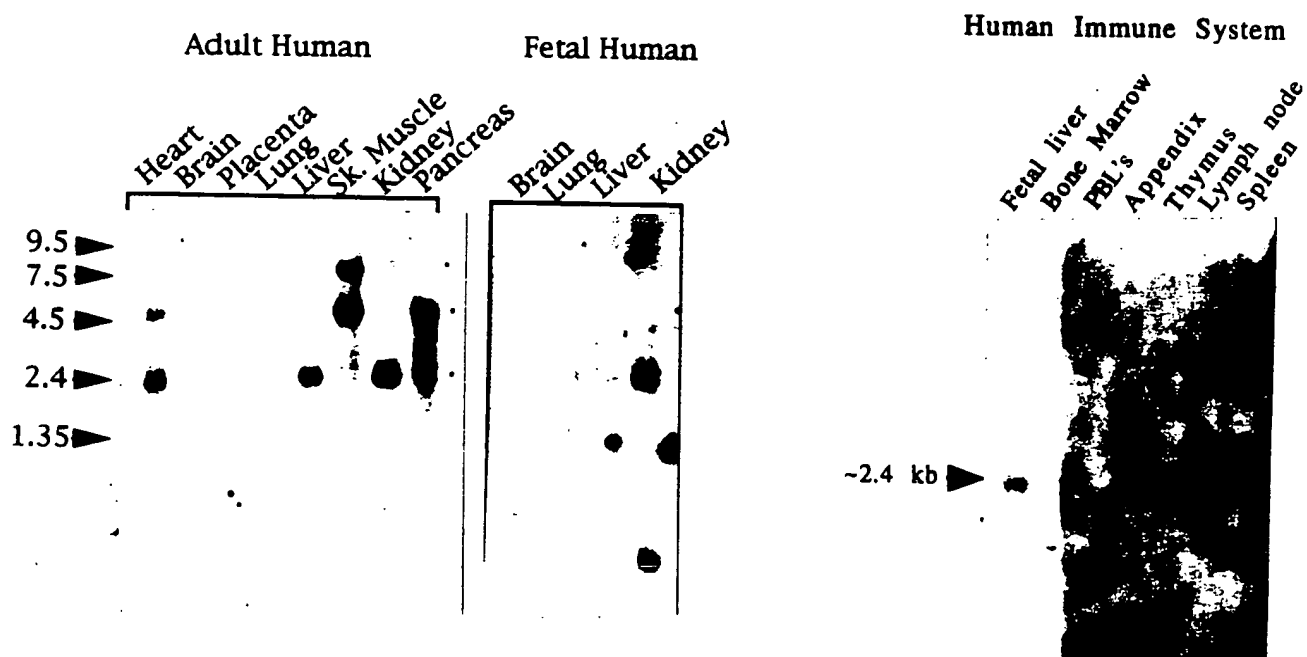
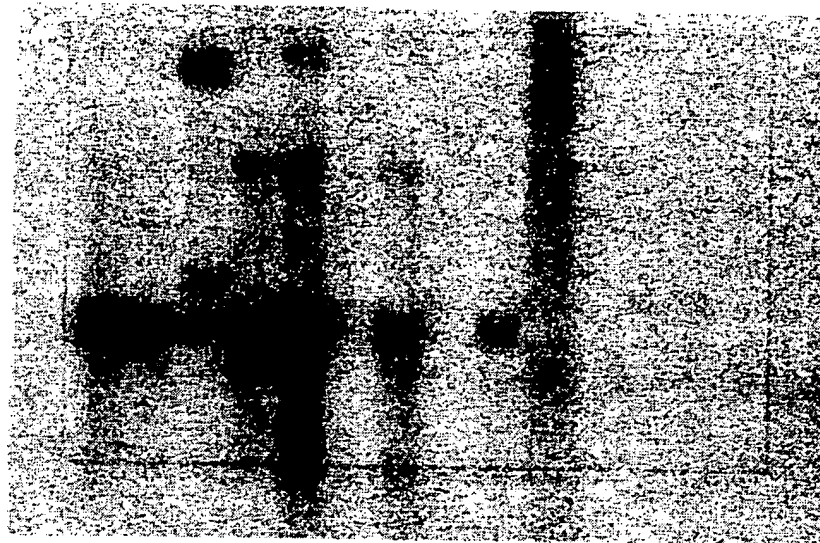


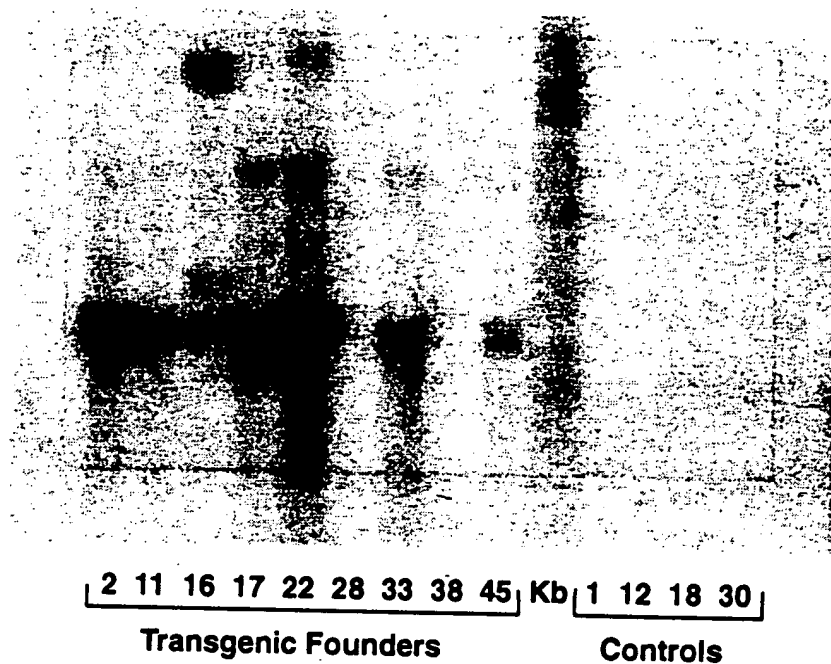
FIGURE 5



2 11 16 17 22 28 33 38 45 Kb 1 12 18 30
Transgenic Founders **Controls**

08974485-11997

FIGURE 5



26677-9877/680

FIGURE 6

PANEL A

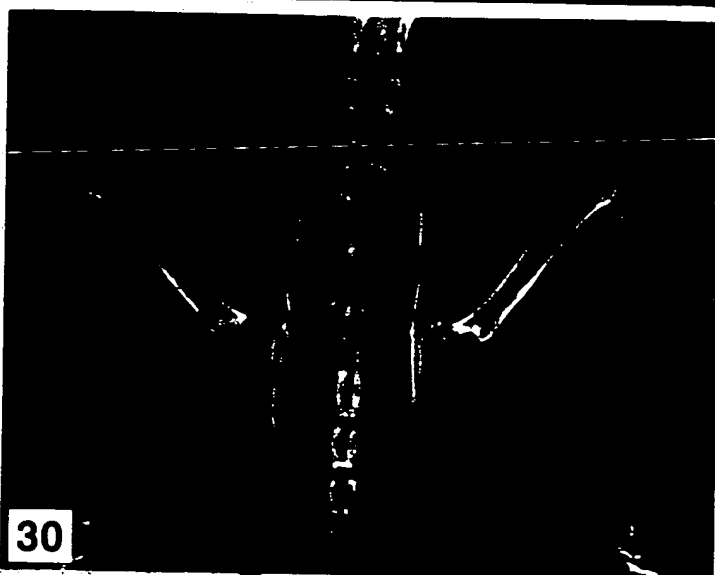
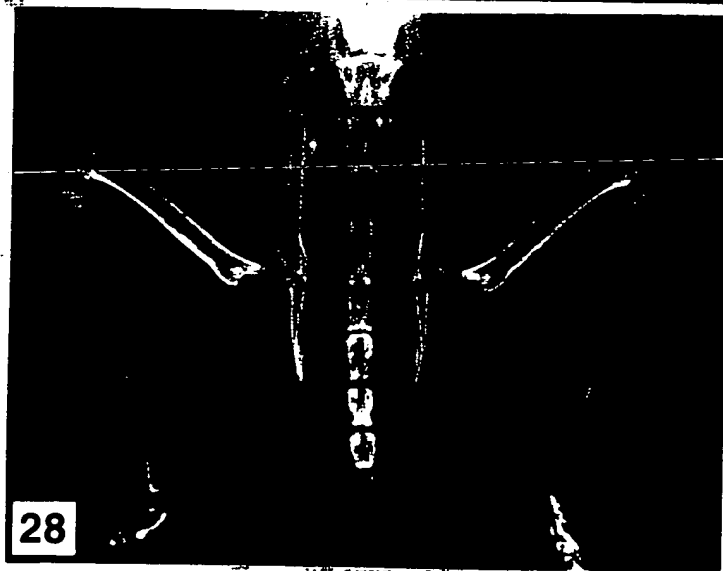
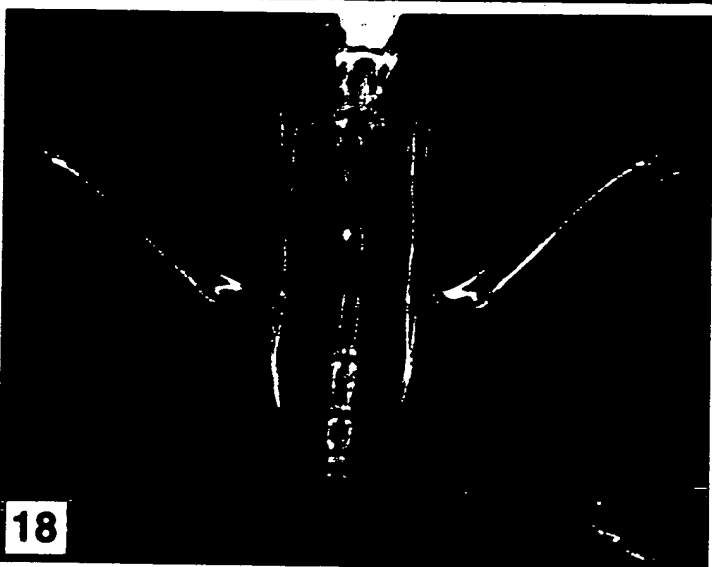
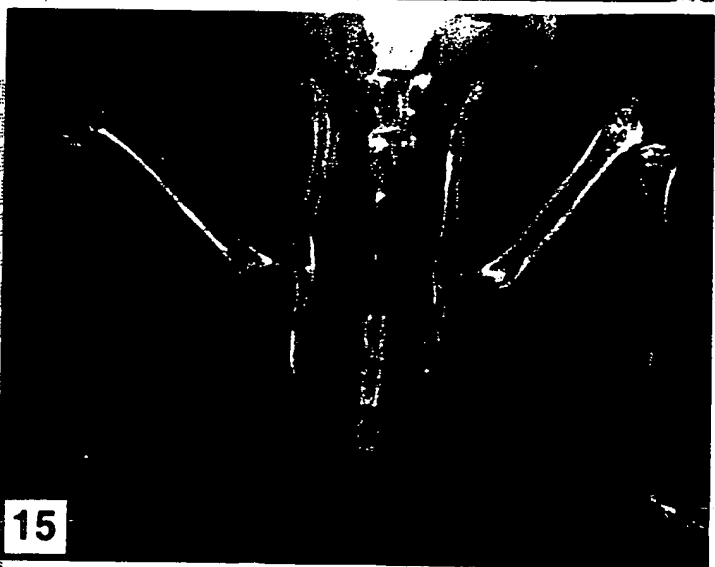
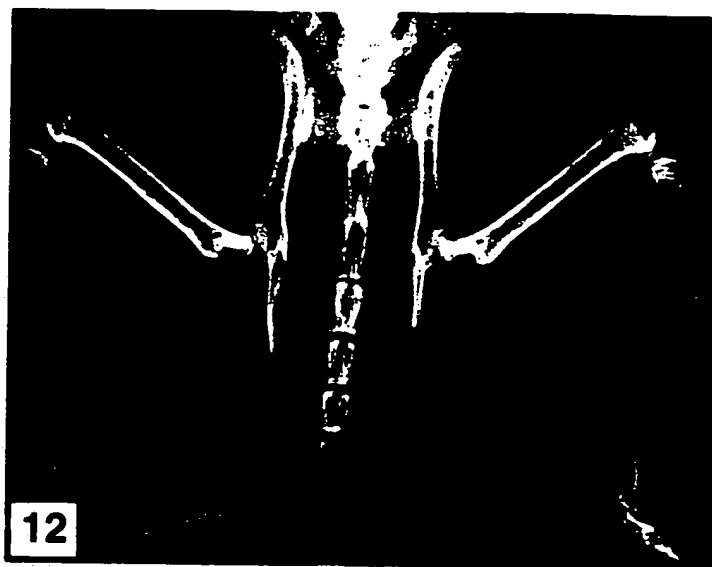
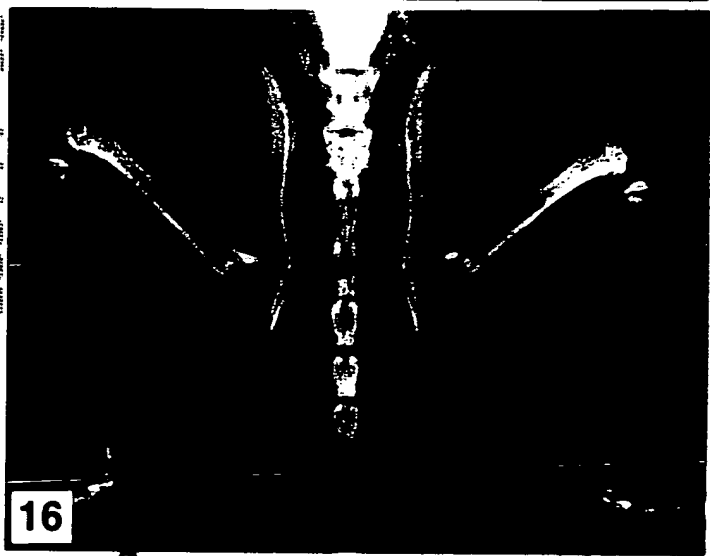
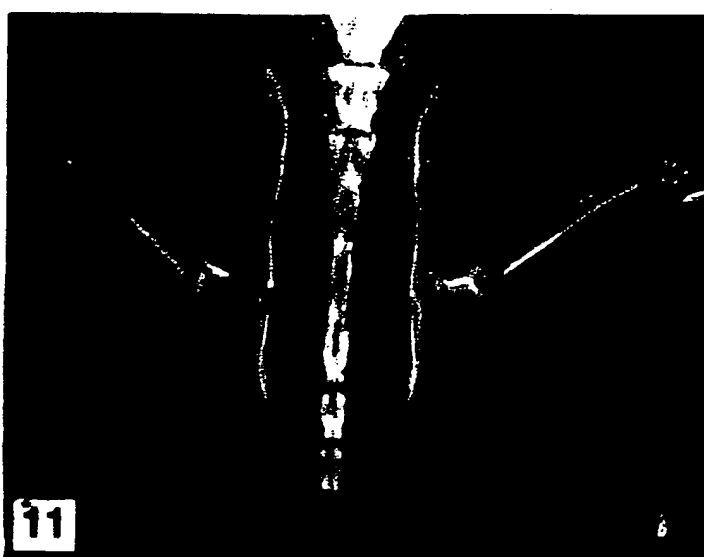
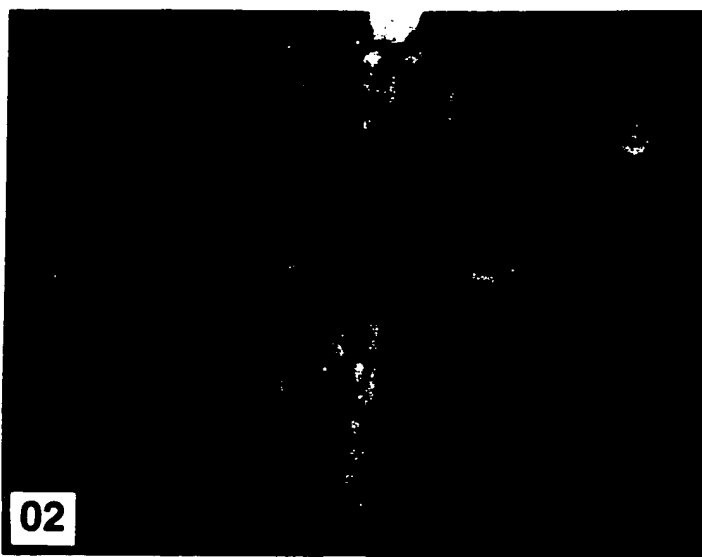


FIGURE 6

PANEL B



08974135-441997

FIGURE 7

PLATE A

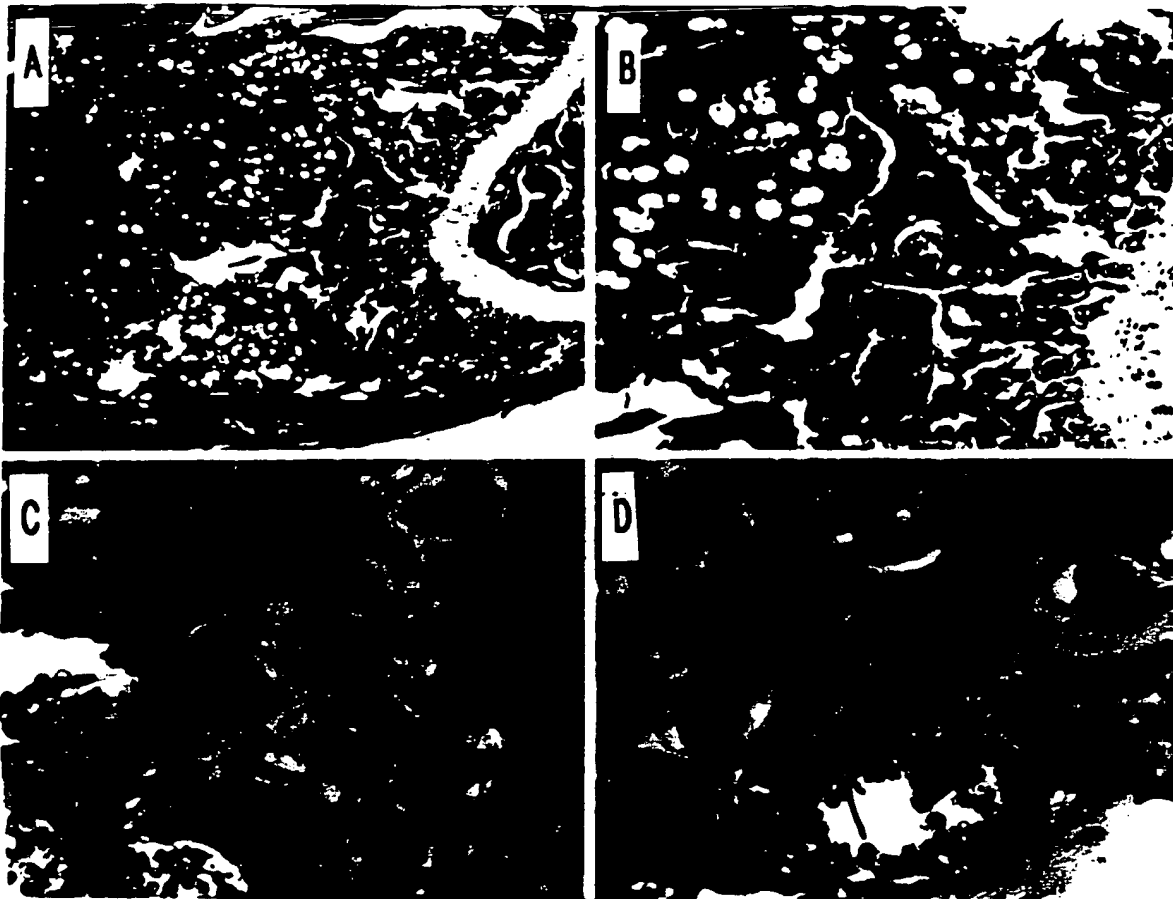
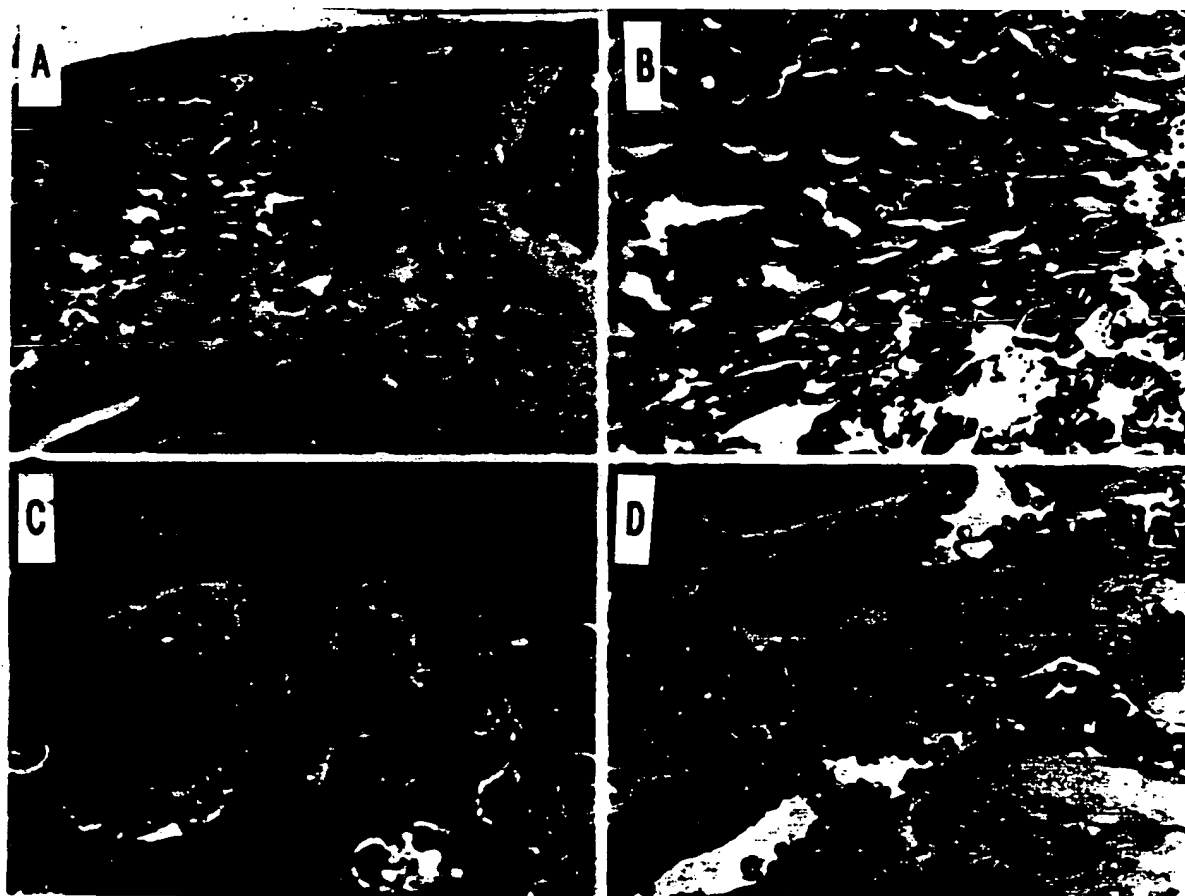
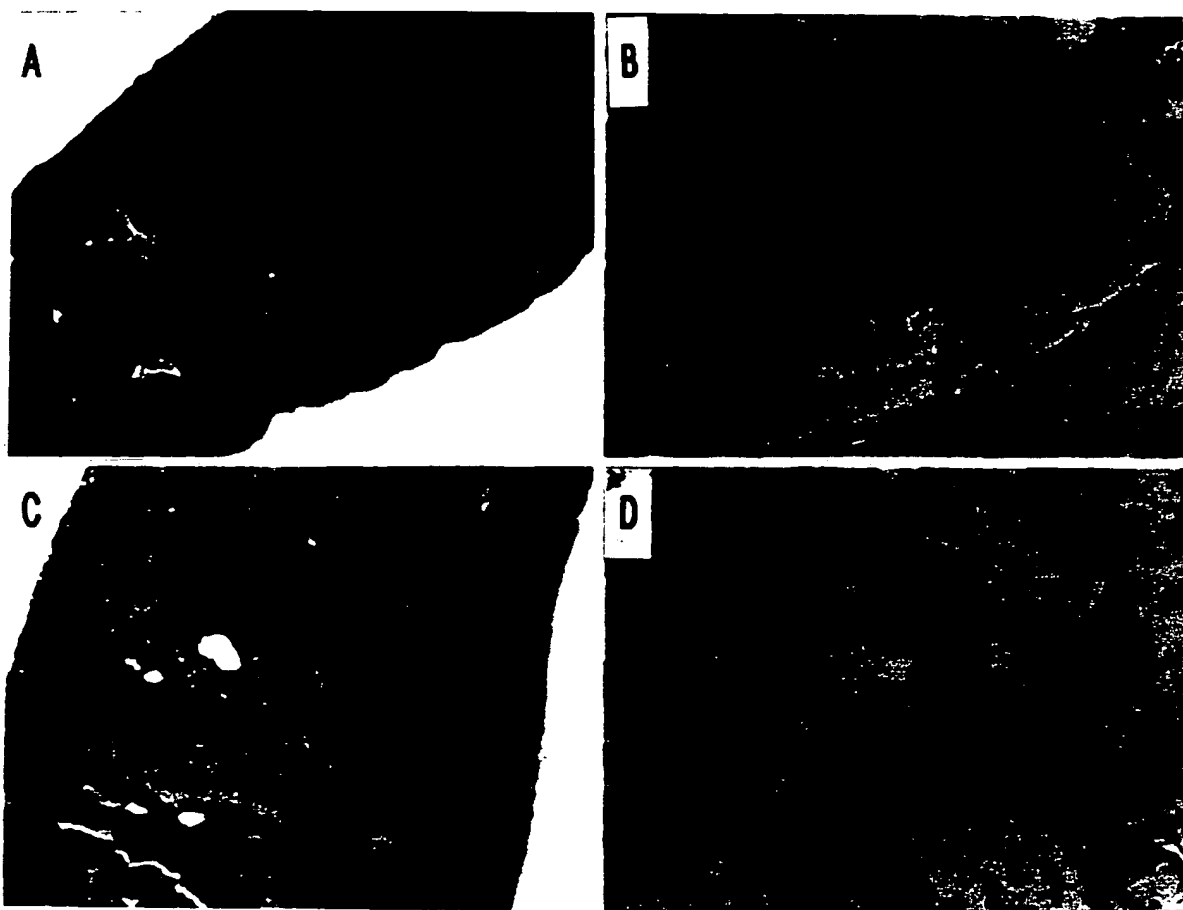


PLATE B



266111-98142680

FIGURE 8



00974486-114997

FIGURE 9A

10 30 50
 CCTTATATAARACGTCATGATTGCCTGGGCTGCAGAGACGCACCTAGCACTGACCCAGCG
 70 90 110
 GCTGCCTCCTGAGGTTTCCCGAGGACCACAATGAACAAGTGGCTGTGCTGCGCACTCCTG
 130 150 170
 GTGCTCCTGGACATCATTGAATGGACAACCCAGGAAACCCCTTCCTCAAAGTACTTGCA
 V L L D I I E W T T O E T L P P K Y L H
 190 210 230
 TATGACCCAGAACTGGTCATCAGCTCCTGTGTGACAAATGTGCTCCTGGCACCTACCTA
 Y D P E T G H Q L L C D K C A P G T Y L
 250 270 290
 AAACAGCACTGCACAGTGAGGAGGAAGACATTGTGTGCCCTTGCCCTGACCACTCTTAT
 K Q H C T V R R K T L C V P C P D H S Y
 310 330 350
 ACGGACAGCTGGCACACCACTGATGATGTGTGTATTGACGCCCAGTGTGCAAGGAACTG
 T D S W H T S D E C V Y C S P V C K E L
 370 390 410
 CAGTCCGTGAAGCAGGAGTGCAACCGCACCCACAACCGAGTGTGTGAGTGTGAGGAAGGG
 Q S V K Q E C M R T H N R V C E C E E G
 430 450 470
 CGTTACCTGGAGATCGAATTCGCTTGAAGCACCGGAGCTGTCCCCCGGGCTCCGGCGTG
 R Y L E I E F C L K H R S C P P G S G V
 490 510 530
 GTGCAAGCTGGAACCCAGAGCGAAACACAGTTTGCAAAAATGTCCAGATGGGTTCTTC
 V Q A G T P E R N T V C K K C P D G F F
 550 570 590
 TCAGGTGAGACTTCATCGAAAGCACCCCTGTATAAACACACGAACTGCAGCACATTGCGC
 S G E T S S K A P C I K H T M C S T F G
 610 630 650
 CTCCTGCTAATTCAGAAAGGAAATGCAACACATGACAAGTGTGTTCGGAACAGAGAA
 L L L I Q K G M A T H D N V C S G N R E
 670 690 710
 GCCACGCAAAAGTGTGAATAGATGTACCCCTGTGTGAAGAGGCCCTTCTTCAGGTTTGCT
 A T Q K C G I D V T L C E E A F F R P A
 730 750 770
 GTTCTTACCAAGATTATACCAATTTGGCTGAGTGTGTTTGGTGGACAGTTTGCCTGGGACC
 V P T K I I P N W L S V L V D S L P G T
 790 810 830
 AAAGTGAATGCGGAGAGTGTAGAGAGGATAAAACGGAGACACAGCTCACAAGAGCAAACC
 K V N A E S V E R I K R R H S S Q E Q T
 850 870 890
 TTCCAGCTGCTGAAGCTGTGGAACATCAAAACAGAGACCAGGAAATGGTGAAGAAGATC
 F Q L L K L W K H Q N R D Q E M V K K I
 910 930 950
 ATCCAAGACATTGACCTCTGTGAAAGCAGCGTGCAGCGGCATCTCGGCCACTCGAACCTC
 I Q D I D L C E S S V Q R H L G H S M L
 970 990 1010
 ACCACAGAGCAGCTTCTTGCTTGTGAGGAGCCTGCCTGGGAAGAAGATCAGCCCAGAA
 T T E Q L L A L M E S L P G K K I S P E
 1030 1050 1070
 GAGATTGAGAGAACGAGAAAGACCTGCAAAATCGAGCGAGCAGCTCCTGAAGCTACTCAGT
 E I E R T R K T C K S S E Q L L K L L S
 1090 1110 1130
 TTATGGAGGATCAAAAAATGGTGACCAAGACACCTTGAAGGGCCTGATGTATGCCCTCAAG
 L W R I K N G D Q D T L K G L M Y A L K
 1150 1170 1190
 CACTTGAAAACATCCCACTTTCCCAAACTGTACCCACAGTCTGAGGAAGACCATGAGG
 H L K T S H P P K T V T H S L R K T M R
 1210 1230 1250
 TTCCTGCACAGCTTCAAAATGTACAGACTGTATCAGAAGCTCTTTTAGAAATGATAGGG
 F L H S P T M Y R L Y Q K L P L E M I G
 1270 1290 1310
 AATCAGGTTCAATCCGTGAAAAATAAGCTGCTTATAACTAGGAATGGTCACTGGGCTGTTT
 N Q V Q S V K I S C L
 CTCA

26974497

FIGURE 9B

10 30 50
 GTATATATAACGTGATGAGCGTACGGGTGCGGAGACGACCGGAGCGCTCGCCAGCCG
 70 90 110
 CGYCTCAAGCCCCTGAGGTTCCGGGGACCACAATGAACAAGTTGCTGTGCTGCGCGCT
 130 150 170
 CGTGTTCCTGGACATCTCCATTAAGTGGACACCCAGGAAACGTTTCCTCCAAAGTACCT
 190 210 230
 TCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCTCCTGGTACCTA
 250 270 290
 CCTAAACAACACTGTACAGCAAAGTGAAGACCGGTGCGCCCTTGCCCTGACCACTA
 310 330 350
 CTACACAGACAGCTGGCACACCACTGACGAGTGTCTATCTGACGCCCCGTGTGCAAGGA
 370 390 410
 GCTGCAGTACGTCAAGCAGGAGTGAATCGCACCCACAACCGCGTGTGCGAATGCAAGGA
 430 450 470
 AGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGCTGCCCCCTGGATTGG
 490 510 530
 AGTGGTGCAAGCTGGAACCCAGAGCGAAATACAGTTTGCAAAAGATGTCAGATGGGTT
 550 570 590
 CTTCTCAAATGAGACGTCTATCTAAAGCACCCCTGTAGAAAACACACAAATGTCAGTGTCTT
 610 630 650
 TGGTCTCTCTGCTAACTCAGAAAGGAAATGCAACACAGCAACATATGTTCCGGAACAG
 670 690 710
 TGAATCAACTCAAAATGTGGAATAGATGTTACCTGTGTGAGGAGGCATTCTTCAGGTT
 730 750 770
 TGCTGTTCCTACAAAGTTTACGCTTAAGTGTCTTAGTGTCTTGGTAGACAATTTGCCTGG
 790 810 830
 CACCAAGATAACGAGAGAGTGTAGAGAGGATAAAACGGCAACACAGCTCACAAGAACA
 850 870 890
 GACTTTCAGCTGCTGAAGTTATGGAACATCAAAACAAGACCAAGATATAGTCAAGAA
 910 930 950
 GATCATCCAAGATATTGACCTCTGTGAAACAGCGTGCAGCGGCACATTGGACATGCTAA
 970 990 1010
 CCTCACCTTCGAGCAGCTTCGTAGCTTGATGGAAGCTTACCGGGAAGAAAGTGGGAGC
 1030 1050 1070
 AGAAGACATTGAAAAACAATAAAGGCATGCAAAACCCAGTGACAGATCCTGAAGCTGCT
 1090 1110 1130
 CAGTTTGTGGCGAATAAAAAATGGCGACCAAGACACCTTGAAGGGCCTAATGCACGCACT
 1150 1170 1190
 AAAGCACTCAAAGACGTACCACTTTCCAAAACGTCACTCAGAGTCTAAAAGAAGACCAT
 1210 1230 1250
 CAGGTTCCTTCACAGCTTCACAATGTACAAATTGTATCAGAAGTTATTTTAGAAATGAT
 1270 1290 1310
 AGGTAACCGGTCATCAGTAAAAATAAGCTGCTTATAACTGGAATGGCCATTGAGCT
 1330 1350
 GTTTCCTCACAATTGGCGAGATCCCATGGATGATAA

00074486-14997

FIGURE 9C

muosteo.frg MNKWLCCALVLLDIIEMWTTQETLPPKYLHYDPETGHOPLLCDKCAPGTYL
 atosteo.frg MNKWLCCALVLLDIIEMWTTQETLPPKYLHYDPETGHOPLLCDKCAPGTYL
 huosteo.frg MNKLLCCALVLLDIIEMWTTQETLPPKYLHYDEETSHOPLLCDKCAPGTYL

muosteo.frg KQHCTVRRKTL CVPCPDHSHSYTDSWHTSDCECVYCSPPVCKEELQSVKQECNRT
 atosteo.frg KQHCTVRRKTL CVPCPDHSHSYTDSWHTSDCECVYCSPPVCKEELQSVKQECNRT
 huosteo.frg KQHCTVRRKTL CVPCPDHSHSYTDSWHTSDCECVYCSPPVCKEELQSVKQECNRT

muosteo.frg HNRVCECEEGGRYLEIEFCLKHRSCPPGSGVVOAGTPERNTVCKKCPDGGFF
 atosteo.frg HNRVCECEEGGRYLEIEFCLKHRSCPPGSGVVOAGTPERNTVCKKCPDGGFF
 huosteo.frg HNRVCECEEGGRYLEIEFCLKHRSCPPGSGVVOAGTPERNTVCKKCPDGGFF

muosteo.frg SGETSSSKAPCIIKHNTNCSSTFGLLLIQKGNATHDNCVCSGNREATOKCGIDVT
 atosteo.frg SGETSSSKAPCIIKHNTNCSSTFGLLLIQKGNATHDNCVCSGNREATOKCGIDVT
 huosteo.frg SNETSSSKAPCRKHTNCSSTFGLLLIQKGNATHDNCVCSGNREATOKCGIDVT

muosteo.frg LCEEAEFFFAVPPTKIIIPNWL SVLVDSLP GTKVNAE SVERIKRRHSSQEOET
 atosteo.frg LCEEAEFFFAVPPTKIIIPNWL SVLVDSLP GTKVNAE SVERIKRRHSSQEOET
 huosteo.frg LCEEAEFFFAVPPTKIIIPNWL SVLVDSLP GTKVNAE SVERIKRRHSSQEOET

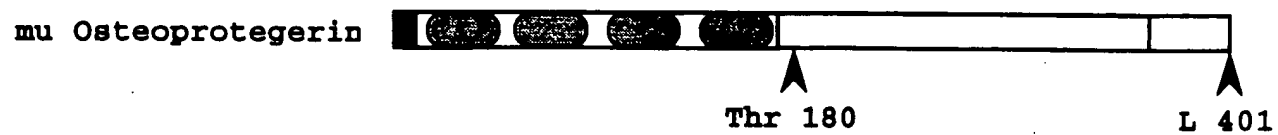
muosteo.frg FQLLKLWKHQNDRDQEMVKKIIQDIDLCESSSVQRHHLGHSNLTTEQLLALME
 atosteo.frg FQLLKLWKHQNDRDQEMVKKIIQDIDLCESSSVQRHHLGHSNLTTEQLLALME
 huosteo.frg FQLLKLWKHQNDRDQEMVKKIIQDIDLCESSSVQRHHLGHSNLTTEQLLALME

muosteo.frg SLPGKKKISPEEIERTRKTKCKSSSEQLLKL LSLWRIKNGDQDTLKGLMYALK
 atosteo.frg SLPGKKKISPEEIERTRKTKCKSSSEQLLKL LSLWRIKNGDQDTLKGLMYALK
 huosteo.frg SLPGKKKISPEEIERTRKTKCKSSSEQLLKL LSLWRIKNGDQDTLKGLMYALK

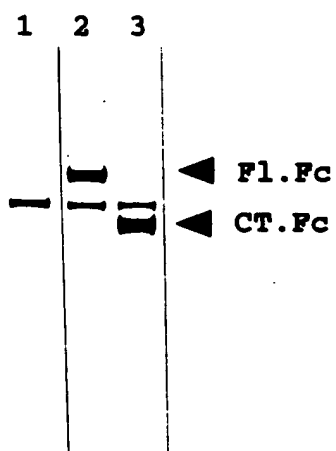
muosteo.frg HLKTSHF PKTVTHSLRKTMRFLHSFTMYRLYO KLFLEMIGNQVQSVKIS C
 atosteo.frg HLKTSHF PKTVTHSLRKTMRFLHSFTMYRLYO KLFLEMIGNQVQSVKIS C
 huosteo.frg HSKTYHFPKTVTHSLRKTMRFLHSFTMYRLYO KLFLEMIGNQVQSVKIS C

muosteo.frg L
 atosteo.frg L
 huosteo.frg L

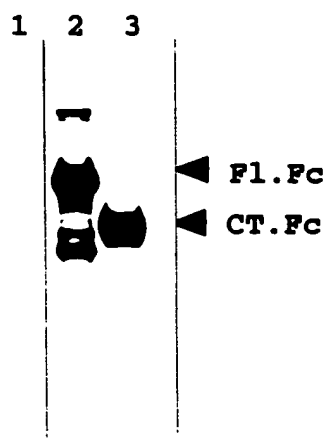
Figure 10A



10B

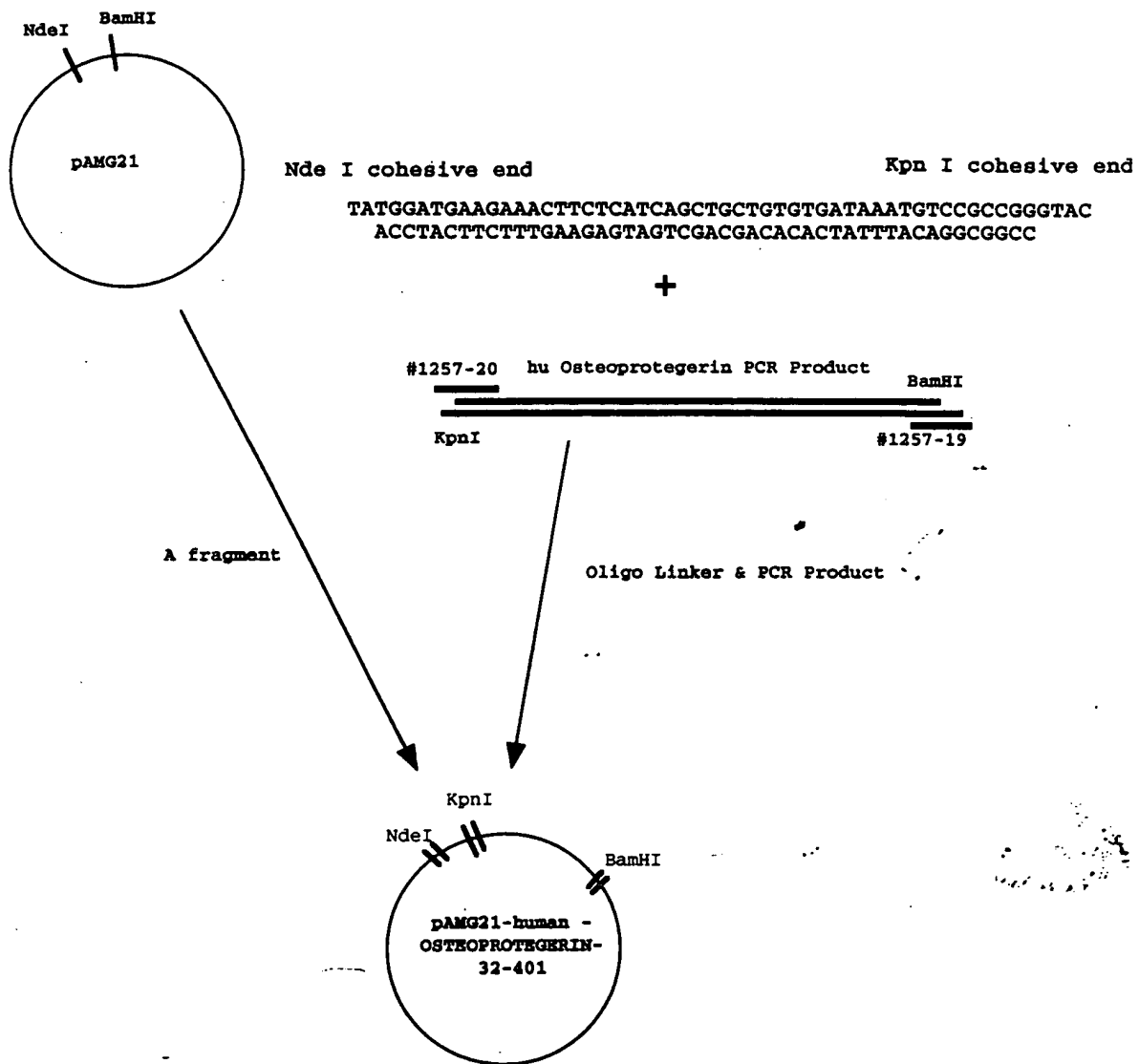


10C



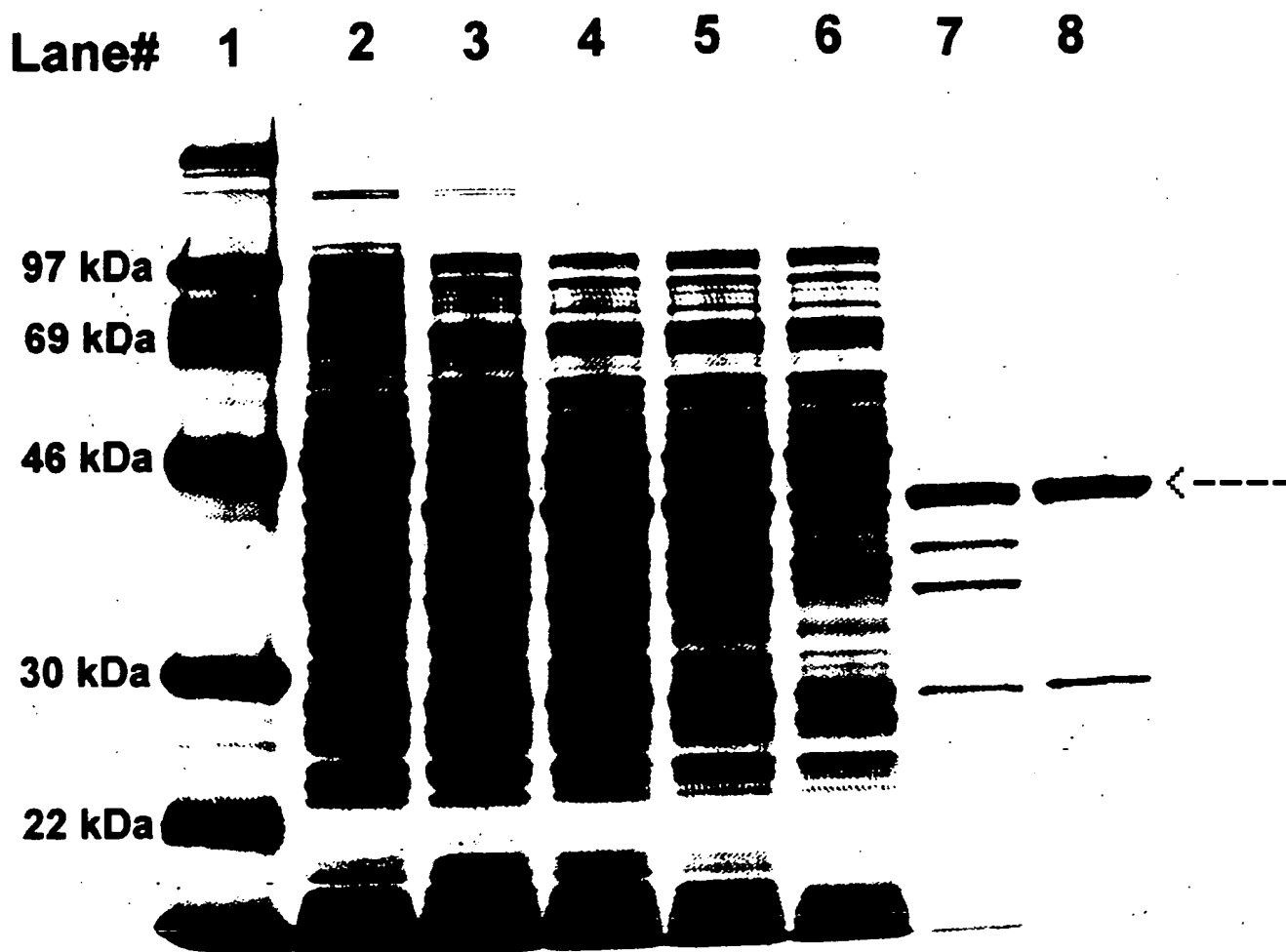
08974185-11997

Figure 11A



089744185-111997

FIGURE 11B



26677-98742680

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☒ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☒ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.